



SEQUENCE LISTING

<110> Pharmacia & Upjohn

<120> Novel Vitamin D Receptor Related Polypeptides, Nucleic Acid Sequence Encoding the Same and Uses Thereof

<130> 10806-65

<140> US 09/143,828

<141> 1998-08-31

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 2905

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: [cDNA of encoding sequence of vitamin D receptor related gamma (VDRRg)]

<400> 1

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<210> 2

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: [Deduced amino
acid sequence of vitamin D receptor related gamma
(VDRRg)]

<400> 2

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Cys Glu Asp Thr Glu Ser Val Pro Gly Lys Pro Ser Val Asn Ala Asp
20 25 30

Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
35 40 45

Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
 50 55 60

Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
 65 70 75 80

Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
 85 90 95

Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile
 100 105 110

Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys
 115 120 125

Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr
 130 135 140

Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys
 145 150 155 160

Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly
 165 170 175

Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser
 180 185 190

Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser
 195 200 205

Leu Lys Val Ser Leu Gln Leu Arg Gly Glu Asp Gly Ser Val Trp Asn
 210 215 220

Tyr Lys Pro Pro Ala Asp Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu
 225 230 235 240

Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser
 245 250 255

Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln
 260 265 270

Ile Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe
 275 280 285

Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu
 290 295 300

Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu
 305 310 315 320

Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His
 325 330 335

Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp
 340 345 350

Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln
 355 360 365

Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro
 370 375 380

Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu
 385 390 395 400

Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
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Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr
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Gly Ser

<210> 3

<211> 2802

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: [cDNA of
 encoding sequence of vitamin D receptor related
 gamma-2 (VDRRg-2)]

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 tgcacagtgc tgcggctgag ttggcttcaa accatccaag aggcccagaa gcaaacctgg 180
 aggtgagacc caaagaaagc tggaaccatg ctgactttgt aactgtgag gacacagagt 240
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<210> 4

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: [Deduced amino acid sequence of vitamin D receptor related

gamma-2 (VDRRg-2)]

<400> 4

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		20						25						30		
Pro	Arg	Gly	Pro	Glu	Ala	Asn	Leu	Glu	Val	Arg	Pro	Lys	Glu	Ser	Trp	
		35					40					45				
Asn	His	Ala	Asp	Phe	Val	His	Cys	Glu	Asp	Thr	Glu	Ser	Val	Pro	Gly	
	50					55					60					
Lys	Pro	Ser	Val	Asn	Ala	Asp	Glu	Glu	Val	Gly	Gly	Pro	Gln	Ile	Cys	
65				70						75					80	
Arg	Val	Cys	Gly	Asp	Lys	Ala	Thr	Gly	Tyr	His	Phe	Asn	Val	Met	Thr	
			85						90					95		
Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ala	Met	Lys	Arg	Asn	Ala	
		100						105						110		
Arg	Leu	Arg	Cys	Pro	Phe	Arg	Lys	Gly	Ala	Cys	Glu	Ile	Thr	Arg	Lys	
	115						120						125			
Thr	Arg	Arg	Gln	Cys	Gln	Ala	Cys	Arg	Leu	Arg	Lys	Cys	Leu	Glu	Ser	
	130					135					140					
Gly	Met	Lys	Lys	Glu	Met	Ile	Met	Ser	Asp	Glu	Ala	Val	Glu	Glu	Arg	
145				150						155					160	
Arg	Ala	Leu	Ile	Lys	Arg	Lys	Lys	Ser	Glu	Arg	Thr	Gly	Thr	Gln	Pro	
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Leu	Gly	Val	Gln	Gly	Leu	Thr	Glu	Glu	Gln	Arg	Met	Met	Ile	Arg	Glu	
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Leu	Met	Asp	Ala	Gln	Met	Lys	Thr	Phe	Asp	Thr	Thr	Phe	Ser	His	Phe	
	195						200					205				
Lys	Asn	Phe	Arg	Leu	Pro	Gly	Val	Leu	Ser	Ser	Gly	Cys	Glu	Leu	Pro	
	210					215					220					
Glu	Ser	Leu	Gln	Ala	Pro	Ser	Arg	Glu	Glu	Ala	Ala	Lys	Trp	Ser	Gln	
225				230						235					240	

Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser Leu Gln Leu Arg Gly	245	250	255
Glu Asp Gly Ser Val Trp Asn Tyr Lys Pro Pro Ala Asp Ser Gly Gly	260	265	270
Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala Asp Met Ser Thr Tyr	275	280	285
Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val Ile Ser Tyr Phe Arg	290	295	300
Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala Phe	305	310	315
Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe Asn Ala Glu Thr Gly	325	330	335
Thr Trp Glu Cys Gly Arg Leu Ser Tyr Cys Leu Glu Asp Thr Ala Gly	340	345	350
Gly Phe Gln Gln Leu Leu Leu Glu Pro Met Leu Lys Phe His Tyr Met	355	360	365
Leu Lys Lys Leu Gln Leu His Glu Glu Glu Tyr Val Leu Met Gln Ala	370	375	380
Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val Leu Gln His Arg Val	385	390	395
Val Asp Gln Leu Gln Glu Gln Phe Ala Ile Thr Leu Lys Ser Tyr Ile	405	410	415
Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe Leu Phe Leu Lys Ile	420	425	430
Met Ala Met Leu Thr Glu Leu Arg Ser Ile Asn Ala Gln His Thr Gln	435	440	445
Arg Leu Leu Arg Ile Gln Asp Ile His Pro Phe Ala Thr Pro Leu Met	450	455	460
Gln Glu Leu Phe Gly Ile Thr Gly Ser	465	470	